

**6030804**

-88	GT	TTGCTCTGGCCAAGTGGCATATTGGAAAGCTTTCTGGAGGGT-29	50
	10	30	
-28	CC	TCTCTTCTACAGCCGGATGGCTCCGGC	90
-8	W L M G S C L L A R A Q L D S D G T	M A W L G A S L H V W	110
	130	150	170
32	GGGGTTGGCTAATGCTCGGCAGGCCAGCTGCCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA		91
12	G W L M G S C L L A R A Q L D S D G T		31
	190	210	230
92	CCATCACTATAGAGGAGGCAGATTGTCTTGCTGAAGCGAAAGTACAATGTGAACTCA		151
32	I T I E E Q I V L K A K V Q C E L N		51
	250	270	290
152	ACATCACAGGCTCAACTCCAGGGAGGAAGGTAATTGTTCCCTGAATGGGATGGACTCA		211
52	I T A Q L Q E G N C F P E W D G L I		71
	310	330	350
212	TTTGGCCAGAGAACAGTGGGAAAATATCGGCCATGCCCTCCTTATATT		271
72	C W P R G T V G K I S A V P C P P Y I Y		91
	370	390	410
272	ATGACTTCAACCATAAGGAGTTGGCTTCCGACACTGTAACCCCAATGGAAACATGGATT		331
92	D F N H K G V A F R H C N P N G T W D F		111
	MATCH WITH FIG. 1B		

FIG. 1A

MATCH WITH FIG. 1A

332	TTATGCACAGCTTAATAAACATGGGCCAATTATTCAAGACTGCCTTCTGCAGC	391
112	M H S L N K T W A N Y S D C L R F L Q P	131
490	CAGATATCAGCATAGGAAGCAAGAACATTCTGTGAACGCCCTATGTAATGGTTG	451
132	D I S I G K Q E F C E R L Y V M Y T V G	151
550	GCTACTCCATCTCTTTGGTCCTGGCTGTGGCTATTCTCATTTGGTTACCTTCAGAC	511
152	Y S I S F G S L A V A I L I I G Y F R R	171
610	GATTGCATTGCACTATCACATGCACTTATTTGTGTCTTTCATGCTGAGAG	571
172	L H C T R N Y I H M H L F V S F M L R A	191
670	CTACAAGCATCTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG	631
192	T S I F V K D R V V H A H I G V K E L E	211
730	AGTC CCTAATAATGCAGGGATGACCCACAAATTCCATTGAGGCAACTCTGTGGACAAAT	691
212	S L I M Q D D P Q N S I E A T S V D K S	231
790		810
		830

**FIG. 1B**

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B

692	CACAATATCGGGTGCAGATTGCTGTTGTGATGTTTACTTCTGGCTACAAATT	751
232	Q Y I G C K I A V V M F I Y F L A T N Y	251
850	870	890
752	ATTATTGGATCCCTGGTGAAGGGTCTACTGCATAATCTCATCTTGTGGCTTCTTT	811
252	Y W I L V E G L Y L H N L I F V A F F S	271
910	930	950
812	CGGACACCAAATACCTGTGGGGCTTCATCTTGATAGGCTGGGGTTCCAGCAGCATTG	871
272	D T K Y L W G F I L I G W G F P A A F V	291
970	990	1010
872	TTGCAGCATGGCTGTGGCACGGCAACTCTGGCTGATGCCAGGTGCTGGGAACCTAGTG	931
292	A A W A V A R A T L A D A R C W E L S A	311
1030	1050	1070
932	CTGGAGACATCAAGTGGATTATCAAGGCACCGATCTTAGCAGCTATTGGCTGAATTTA	991
312	G D I K W I Y Q A P I L A A I G L N F I	331
1090	1110	1130
992	TTCTGTTCTGAATAACGGTTAGAGTCTAGCTACCAAAATCTGGAGACCAATGCAGTTG	1051
332	L F L N T V R V L A T K I W E T N A V G	351
1150	1170	1190
1052	GGCATGACACAAGGAAGCAAATACAGGAAACTGGCCAAATCGACACTGGCTGGTCCCTAG	1111
352	H D T R K Q Y R K L A K S T L V L V	371

FIG. 1C

MATCH WITH FIG. 1C

1112	TCTTTGGAGTGCATTACATCGTGTTCGCTGCCTCACTCCTTCACTGGGCTGGT	1171	
372	F V H Y I V F V C L P H S F T G L G W	391	
1270	1230	1250	
1172	GGGAGATCCGCATGCACTGTGAGCTCTTCAACTCCCTTCAGGGTTCTAGGGTTCTGTCTA	1231	
392	E I R M H C E L F F N S F Q G F V S I	411	
1330	1290	1310	
1232	TCATCTACTGCTACTGCAATGGAGAGGTTCAAGGGAGGGTGAAGAAGATGTGGAGTCGGT	1291	
412	I Y C Y C N G E V Q A E V K M W S R W	431	
1390	1350	1370	
1292	GGAATCTCTCGTGGACTGGAAAAGGACACCCGCCATGTGGCAGCCAGATGCCAGATGGGGCTCAG	1351	
432	N L S V D W K R T P P C G S R R C G S V	451	
1450	1410	1430	
1352	TGCTCACCCGTGACGGCACAGCACAGCAGTCAACAGGTGGGGCAGCACACGGCAT	1411	
452	L T T V T H S T S Q S Q V A A H A W	471	
1510	1530	1550	
1412	GGTGCCTATCTGGCAAAGCTGCCAAGATGCCAGCACAGCTGACAGCCACATCAC	1471	
472	C L S L A K L P R S P A D S L T A T S L	491	

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

1570	1590	1610
1472 TTTACCTGGCTATGTCGGAGTAACCTCAGGCCAGGA 492 Y L A M S G V T Q S R T A S H T L S T R		CACACACTCTCCACCGA
1630	1650	1670
1532 GGAGCAACAAGGAAGATAAGTGGGAGGCAGAGAGATG 512 S N K E D S G R Q R D D I L M E K P S R		ATGGAGAACGGCCTTCCA
1690	1710	1730
1592 GGCCTATGGAATTCAACCCAGACACTGAAGGGATGACA 532 P M E S N P D T E G		AGGAAACTGAGGATGTTCCT
1750	1770	1790
1652 GAATGGACATGTTGGCTGACTTTCATGGGCTGGCCA 1712 TGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAA 1772 TAATAGTTTAACTGAAATTGGCTCCATGAATTGGCAT 1832 TGTCAATTGGAGTAGTTTACCTTCTATTGGCATCAAG 1892 GGTATTGGCTCTGTTGATTGGTCA		ATGGCTGGTGTGAGAGGGC
1810	1830	1850
		AAGGTGTTACTTAA
1870	1890	1910
		AAACTAACGACATGAAAATGCAAG
1930	1950	1970
		TTAAATTAAATGTAT
1990		
		1891
		1914

**FIG. 1E**

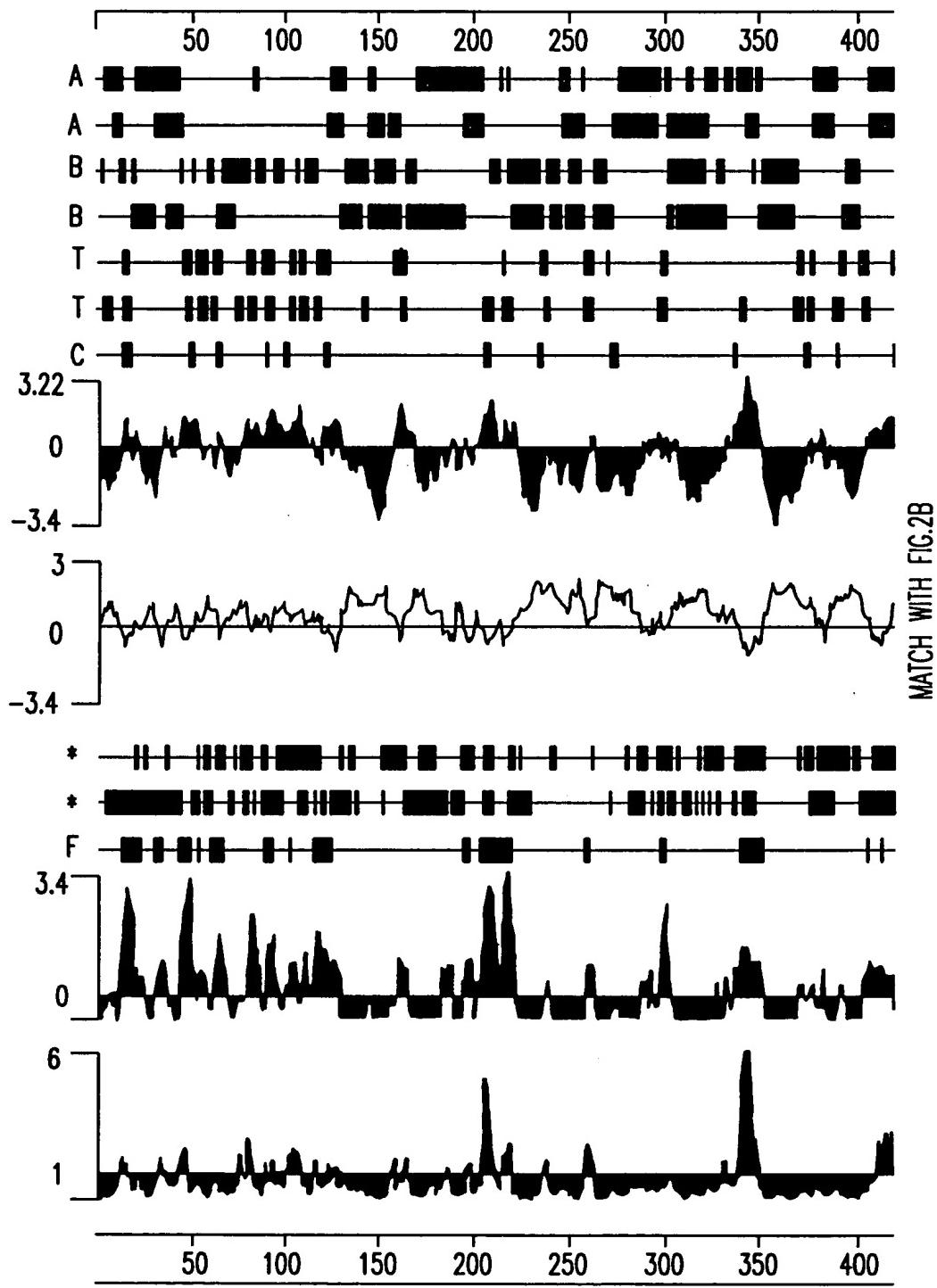
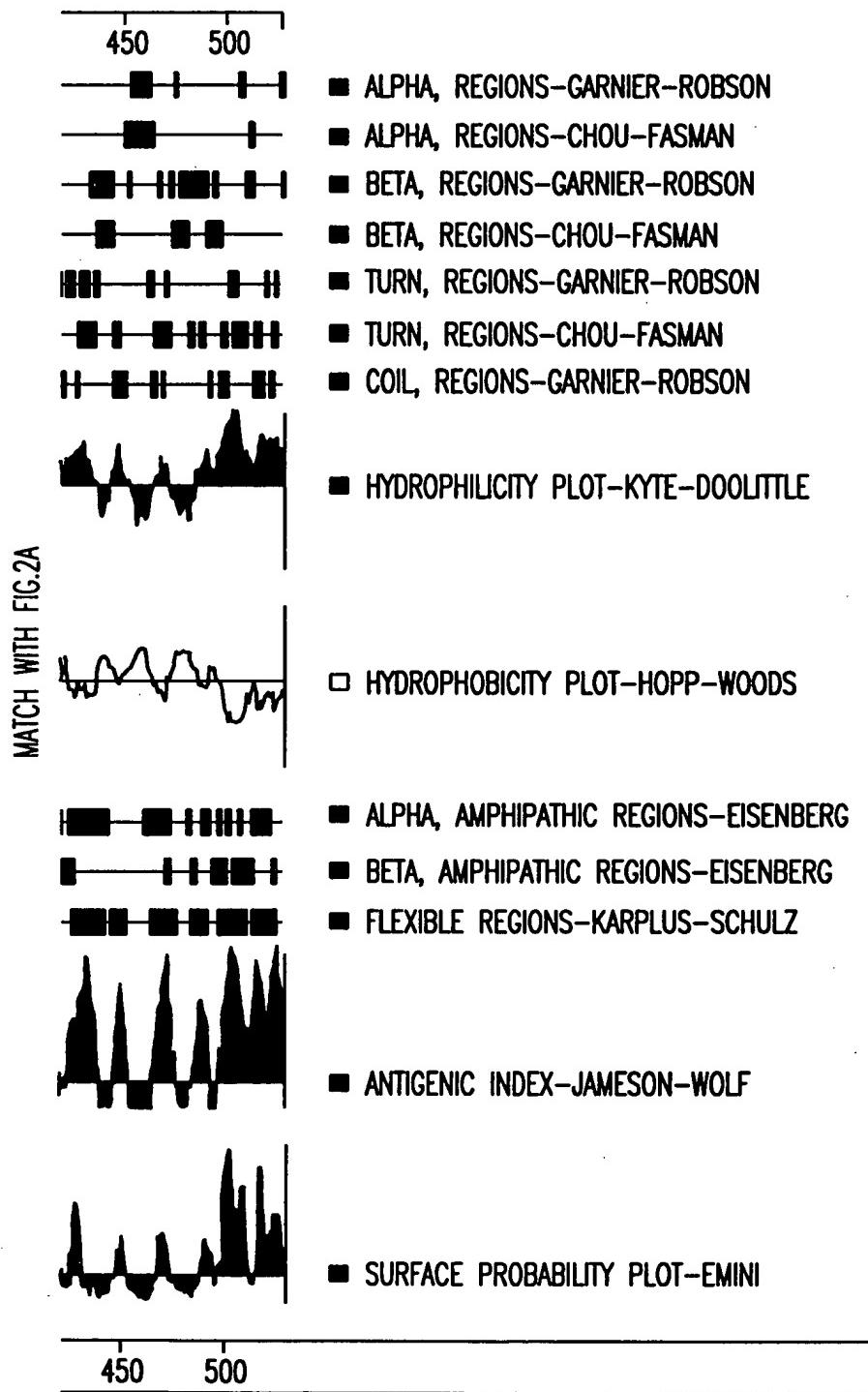


FIG. 2A



**FIG. 2B**

Sequences producing High-scoring Segment Pairs:

		Reading	High	Probability	N
		Frame	Score	P(N)	
gp M74445 OPOPTHR_1	parathyroid hormone receptor [Didelphis virginiana]	+3	597	8.2e-204	6
pir S A39286	parathyroid hormone / parathyroid hormone receptor [Didelphis virginiana]	+3	597	2.9e-203	6
gp L04308 HDMPTHR_1	parathyroid hormone receptor [Didelphis virginiana]	+3	580	6.7e-190	5
pir S S29610	parathyroid hormone receptor - hormone receptor [Didelphis virginiana]	+3	580	6.1e-189	5
gp M77184 RATPATHR_1	parathyroid hormone receptor [Rattus norvegicus]	+3	576	7.7e-188	5
gp X78936 MMPHRPR_1	parathyroid hormone/parathyroid hormone receptor [Mus musculus]	+3	576	7.7e-188	5
pir S A42698	parathyroid hormone and parathyroid hormone receptor [Mus musculus]	+3	576	7.7e-188	5
gp L34611 MUSPTHRO6_1	parathyroid hormone/parathyroid hormone receptor [Mus musculus]	+3	576	4.1e-174	5
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 [Homo sapiens]	+3	319	1.2e-98	5
gp M86835 RATVASREC_1	vasoactive intestinal polypeptide [Rattus norvegicus]	+3	254	3.1e-91	5

**WARNING:** Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTHR\_1 parathyroid hormone receptor [Didelphis virginiana]  
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

**FIG. 3A**

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSVDKSQYIGCKIAVVMFIYFLATNYWILVEGLYLHNLLIFVAFFSDT 908  
I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+  
Sbjct: 253 ITEEEELRAFTEPPADKAGFVGCRVAVTVFLYFLTTNYWILVEGLYLHSLIMAFFSEK 312

Query: 909 KYLMGFILLIGWGFPAAFAVVAARATLADARCWELSAGDIRKIYQAPILAAGICLNFILE 1088  
KYLMGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILE  
Sbjct: 313 KYLMGFITLFGWGGLPAVFWVATLANTECWDLSGGNKKWIIQVPILAAIVVNFILE 372

Query: 1089 INTVRVLATKIKIWEETNAVGHDTRKQYRKLAESTLVLVLVFGVHYIVFVCLPHS 1244  
+N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++  
Sbjct: 373 INTIIRVLATKIKRETNAGRCDTTRQYRKLLKSTLVLMPLEFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPPEWDGLICWPRGTVGKISAWPCPPYYIDFNHKGVAFRHNCNPNGTNDFMHSLNKTN 446  
+G C PEWD +CWP G GK+ AVPCP YYIDFNHKG A+R C+ NG+W+ + N+TN  
Sbjct: 102 DGFCCLPEWDNTIVCWPAGVPGKVVAWPCPDYIYDENHKGRAYRRCDSNGSWELVPGANRTW 161

Query: 447 ANYSDCLRFL 476  
ANY S+C++FL  
Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLYVVMYTGYESISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSMILRATSIFV 677  
+E +RL ++YI+GYFRRLLHCTRNYIHMHLFVSMILRA SIF+  
Match with FIG. 3 C

FIG. 3B

MATCH WITH FIG. 3B

Sbjct: 177 EREVDRUGMIIYTGVYSISIGSLTVAVLILGYFRRLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESLIMQD 740  
KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNSFQGFFVSIIYCYCNGEVQAETVKKMWSRWNLSDWKRTPPCGS 1424  
+G+ W+++MH E+ FNSFQGFFV+ IITYC+CNGEVQAEE+KK WSRW L++D+KR GS  
Sbjct: 427 SGILWQVQMHYEMLFNSFQGFFVAI IYCFNCNGEVQAEEIKKSWSRWTLAIIDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQUDSDGTITIEEQIVLVLKAKVQCELNITAQLQEGER 269  
A +D+D IT EEQI+L+ A+ QCE + L+ E  
Sbjct: 24 ALWDADDVTITKEEQILLRNAQAQCEQRLKETVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204  
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISCKAAKIASRQPDSHITLPGYV 1576  
+S + A A + H LPGYV  
Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C